Sequence

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US-09-170-496D-206
US-09-745-842-17
US-09-745-842-15
US-09-102-710B-3
US-08-102-710B-3
US-08-813-974B-373
US-08-813-974B-2
US-08-442-1134A-2
US-08-446-08BA-2
US-08-445-81B-2
US-08-445-103-3
US-08-749-707-3
US-09-947-922-3
US-09-947-922-3
US-09-097-938-6
US-08-772-84-00-6
US-08-772-84-06-6
US-08-772-84-06-6
US-08-772-84-06
  August 20, 2005, 11:04:48; Search time 161 Seconds (without alignments) 153.007 Million cell updates/sec
                                                                                            1712
1 MEPNGTFSNNNSRNCTIENF.......KAKTKCVFPVSVWLRKETRV 330
         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                          513545 seqs, 74649064 residues
                                       - protein search, using sw model
                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                     US-09-826-791A-2
                 Copyright
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206, App 2, App 17, Appl 15, Appl 3, Appl 2, Appl 2, Appl 3, Appl 3, Appl 3, Appl 3, Appl 6, Appl 6, Appl 6, Appli 6, Appli 6, Appli

Sequence Seq

ALIGNMENTS

Fotal number of hits satisfying chosen parameters:

score:

Perfect

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

60 60 76 1130 1196 2240	300
BEBUILT US-09-585-876-2 Sequence 2, Application US/09585876 Sequence 2, Application US/09585876 Sequence 2, Application US/09585876 Sequence 3, Application US/09585876 Sequence 3, Application US/09585876 Sequence 4, Application Independent	Oy 241 FLCFLPYHTLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYPAGENFKDRL 3

Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 44, Appli Sequence 44, Appli Sequence 44, Appli Sequence 32, Appli Sequence 32, Appli Sequence 24, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

Description

В

Length

Query

Result No.

Sequence 374, Sequence 14, A Sequence 4, Apl

US-09-585-876-2
US-09-044-404h-2
US-09-044-404h-2
US-09-153-848-44
US-09-29-84-13
US-09-29-843h-44
US-09-29-843h-44
US-09-170-496D-32
PCT-US93-11153-44
PCT-US93-11153-44
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US-09-170-496D-184
US-09-170-496D-184
US-09-170-496D-184
US-08-185-818-4
US-09-170-496D-184
US-08-185-818-4

4440 4440 4440 39440 4440 4439 4439 4377

Sequence 4 Sequence 4 Sequence 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Issued P(Cents AA:*

(cgn2_b/todata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330

301

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374, App 14, App 14, Appl 4, Appli 4, Appli 4, Appli 78, Appli 78, Appli 4, Appli 17, Appli 17, Appli 30, Appli 8, Appli 8, Appli 8, Appli 8, Appli 8, Appli 8, Appli 90, Appli 8, Appli 90, Appli 90, Appli 90, Appli 90, Appli 90, Appli

Sequence 4, 7 Sequence 78, Sequence 4, 7

Sequence

Sequence 4, 7 Sequence 17, Sequence 30, Sequence 30,

Sequence (Sequence (

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248 PYHIQRTIHLHFLHNETKPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL- 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVVWYSSIYFLTVLSVVRFLAMVHPF 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 NYIALVVGCLLPPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 PYHIQRTIHLHFLHRETKPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL- 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 SSATCHDTIDDFRNQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVAD 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Gaps
                                                                                                                                                                                                                                                                          APPLICANT: SATHE, GANESH M.
APPLICANT: BALSEY, WENDY
APPLICANT: ELLIS, CATHERINE E.
APPLICANT: APRES, CATHERINE E.
APPLICANT: POLEY, JAMES, U.
APPLICANT: POLEY, JAMES, J.
APPLICANT: SARAU, HENRY M.
APPLICANT: CHAMBERS, J.
APPLICANT: CHAMBERS, JONA CLONE HMTMEBI THAT ENCODES A NOVEL
TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
FILE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
FILE REFERENCE: GH-70001-1.DJ
CURRENT FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 09/044,404
PRIOR APPLICATION NUMBER: 09/044,404
PRIOR PLING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 08/44,404
PRIOR FILING DATE: 1997-04-22
NUMBER: OS ESQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.7%; Score 559; DB 4; Length 33 38.0%; Pred. No. 7.7e-36; Live 71; Mismatches 106; Indels
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FastSEQ for Windows Version 3.0
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Patent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
                                                                                                                                                                                                     Sequence 2, Application US/09586924
Patent No. 6506878
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 38.0%
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: HOMO SAPIENS
                                              302 SALRK 306
                                                                                             307 STFRK 311
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SEQ ID NO 2
LENGTH: 337
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US-09-586-924-2
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A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.7%; Score 559; DB 3; Length 337; 38.0%; Pred. No. 7.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOCTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,404A
FILING DATE: MARCH 19, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,795
FILING DATE: ARRIL 22, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
NAME: Han, William T.
REGISTRATION NUMBER: 34,344
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             E: SmithKline Beecham Corporation 790 Swedeland Road, P.O. Box 1539
                                                             Sequence 2. Application US/09044404A
Patent No. 620075
GENERAL INFORMATION:
APPLICANT: BALNEY, WENDY
APPLICANT: ELLIS, CATHERINE
APPLICANT: AMES, ROBERT
APPLICANT: FOLEY, JAMES
APPLICANT: FOLEY, JAMES
APPLICANT: SARAU, HENRY
APPLICANT: SARAU, TITLE OF INVENTION: ANOVEL HUMAN
TITLE OF INVENTION: A NOVEL HUMAN
TITLE OF INVENTION: A NOVEL HUMAN 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 790 Swedeland
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                        RESULT 2
US-09-044-404A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-044-404A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLLDSGSEQNGSVTSCLELNLYKIAKLQT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIIITLIIFF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
No. 5759804el Seven Transmembrane Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 479; DB 1; Length 339;
Pred. No. 1.2e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62; Mismatches 126; Indels
                                                                                           STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                       ADDRESSEE: Marehall, O'Toole, Gerstein, Murray ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                              PILING DATE:
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REPERSNEY/COCKET NUMBER: 31794
TELECOMMUNICATION: TRFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRLKSAL----RKGHPQKAKTK 315
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                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.0%;
34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 339 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 34.84
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-153-848-44
                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
  TITLE OF INVENTION:
                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298
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246 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305
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APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCE: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.0%; Score 479; DB 2; Length 339; ilarity 34.8%; Pred. No. 1.2e-29; Conservative 62; Mismatches 126; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: FILING DATA:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-05
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 992700
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Matches 112; Conserv
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RESULT 6 US-09-299-843A-44

US-08-812-871-3
; Sequence 3, Application US/08812871
; Patent No. 5955303
; GENERAL INFORMATION:
APPLICANT: Au-Young, Janice

us-09-826-791a-2.rai

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ZIP: 60606
COMPUTER READABLE FORM:
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Matches 112; Conservative
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STATE: Illinois
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Sequence 44, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Goddiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSE: 66
ADDRESSEE: BOARSHII, O'Toole, Gerstein, Murray & ADDRESSEE: BOARSHII, O'Toole, Gerstein, Murray & ADDRESSEE: BOARSHII, O'Toole, Gerstein, Murray & ADDRESSEE: BOARSHIII, O'Toole, Gerstein, Murray & ADDRESSEE BOARSHIIII, O'Toole, Gerstein, Murray & ADDRESSEE BOARSHIII, O'Toole, Gerstein, Murray & ADDRESSEE BOARSHII BOARSHIII BOARSHIII BOARSHII BOARSH
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28.0%; Score 479; DB 3; Length 339;
Best Local Similarity 34.8%; Pred. No. 1.2e-29;
Matches 112; Conservative 62; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
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REFERENCE/DOCKET NUMBER: 27866/32059B
REFERENCE/COCKET NUMBER: 27866/32059B
TELECOMMULICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION ATT.
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATE:
PRIOR APPLICATION DATE:
FILING DATE: 17-NOV-1993
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APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein
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CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 FSNNNSRNCTIEN-FKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA 65
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                                                                                                                                                                                                                                               APPLICANT: Godiska, Ronald
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: NO. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-3378-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: NO. 6348574and, Greta E. REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 31794 TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 474-6300 TELEFAX: (312) 474-0448
298 DRLKSAL----RKGHPQKAKTK 315
                                           306 HALCNLLCGKRLKGPPPSFEGK 327
                                                                                                                                                                   Sequence 44, Application US/09088337B Patent No. 6348574 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
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LENGTH: 339 amino acids
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66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
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; Pred. No. 1.2e-29;
62; Mismatches 126; Indels
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APPLICANT: GCAYNE, JEANINE D
APPLICANT: GCAYNE, STEVEN M
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298 DRLKSAL----RKGHPQKAKTK 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
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Best Local Similarity 34.8%
Matches 112; Conservative
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                                                                                                   ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy
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                       CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Behan, Dominic P.
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
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  192 HALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVRMIAIVLAIFL 245
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APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
APPLICANT: Schweikart, Vicki L.
APPLICANT: Schweikart, Voki L.
APPLICANT: Schweikart, Vicki L.
APPLICANT: Schweikart, Vicki L.
ANDRER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US93-11153-44; Sequence 44, Application PC/TUS9311153; GENERAL INFORMATION:
                                                                                                                                                     298 DRLKSAL----RKGHPQKAKTK 315
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                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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US-09-170-496D-32
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LENGTH: 339
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                                                                                                                                                                                                                                                                     Query Match 27.8%; Score 476; DB 4; Length 339; Best Local Similarity 34.8%; Pred. No. 2e-29; Matches 112; Conservative 61; Mismatches 127; Indels
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Patent No. 6114139

GENERAL INFORMATION:
APPLICANT: Homowa, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Pujii, Ryo
APPLICANT: Pujii, Ryo
APPLICANT: Pujii, Ryo
APPLICANT: Pujii, Ryo
APPLICANT: Ohdik, Tetsuya
APPLICANT: Ohdik, Tetsuya
APPLICANT: Ohdik, Tetsuya
APPLICANT: Ohdik, Shoji
APPLICANT: Ohdik, Sh
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
           SOFTWARE: Patentin version 3.1
                                                                                                                                                        ORGANISM: Homo sapiens
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                                          SEQ ID NO 182
LENGTH: 339
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Patent No. 6555339

GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: NO. 6555339-Endogenous, Constitutively Activated Human G Protein-TITLE OF INVENTION: NUMBER: US/09/170,496D

CURRENT APPLICATION UNMBER: US/09/170,496D

CURRENT FILING DATE: 1998-10-13

NUMBER OF SEQ ID NOS: 294
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                                                                                                                                                                                                  CAPTER READABLE FORM:

MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTONENY/AGENT INFORMATION:
NAME: MULLINS, J.G
REGISTRATION NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
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US-09-170-496D-182
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APPLICANT: Gantzen, Hans-Michael
APPLICANT: Ramakrishnan-DuBridge, Vanitha
APPLICANT: Gullius, David
APPLICANT: Hollopeter, Gunter
APPLICANT: Hollopeter, Gunter
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: P2712 Receptor
TITLE OF INVENTION: P2712 Receptor
FILE REFERENCE: 44481-5053-US
CURRENT APPLICATION NUMBER: US/09/745,842
CURRENT FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 14
LENGTH: 373
TYPE: PRT
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   Sequence 14, Application US/09745842
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324 YFLAGDTFRRRLSRATRK 341
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                                                                                                      Conley, Pamela B.
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Matches 102; Conservative
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                                                                                                                                                                                 PILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 02-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
APPLICATION NUMBER: JP 6-189272
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PRIOR APPLICATION DATA:
APPLICATION NATA:
UMBER: JP 7-057186
16-MAR-1995
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ATTORNEY/AGENT INFORMATION:
NAME: REGISTRATION NUMBER: 34,235
REGISTRATION NUMBER: 4575:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-533-3400
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INFORMATION FOR SEQ ID NO: 374:
SEQUENCE CHARACTERISTICS:
                                                                                                                                   20-JAN-1995
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amino acid
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                               FILING DATE: 16-MAR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                               FILING DATE: 20-JAN-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Best Local Similarity
Matches 98; Conserv
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RESULT 13 US-09-745-842-14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LAISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLA 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 MVHPFRLLHVTSIRSAWILCGIIW-ILIMASSIMLLDSGS--EQNGSVTSCLE----L 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 TPSNNNSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLN
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                                                                                                                                                                                                                                                                                   Length 373;
                                                                                                                                                                                                                                                                          26.1%; Score 446; DB 4; Length 37 32.1%; Pred. No. 4.5e-27; ive 79; Mismatches 111; Indels
OTHER INFORMATION: P2Y1 purinergic receptor; p2yr
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US-08-559-524A-4
Sequence 4, Application US/08559524A
Patent No. 5871963
GENERAL INFORMATION:
APPLICANT: Conley, Pamela B.
APPLICANT: Conley, Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
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MEDIUM TYPE: Floppy disk
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LENGTH:
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               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PPPLICATION NUMBER: US/08/559,524A
FILING DATE: 15-NOV-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C.
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-08-749-707-4
Sequence 4, Application US/08749707
Patent No. 6063582
GENERAL INFORMATION: Pamela B.
APPLICANT: Jantzen, Hans-Michael
TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGIGYRATION NUMBER: 30,988
REGIGYRATION NUMBER: 044481-5010-00-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: MORGAN, LEWIS & BOCKIUS LLP
1800 M Street, N.W.
PC-DOS/MS-DOS
                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               LENGTH: 373 amino acids
TYPE: amino acid
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.8%; Score 442; DB 3; Length 37 Best Local Similarity 31.0%; Pred. No. 9.1e-27; Matches 95; Conservative 78; Mismatches 109; Indels
                                                                                                                                         044481-5010-01-US
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APPLICATION NUMBER: US/08/749,707
                                                                                                                30,988
                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 202-467-7000
                                                                                                                                                                                                           TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                   15-NOV-1996
                                                               ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
                                                                                          NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                    373 amino acids
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 KSALRK 306
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                      FILING DATE: 15
CLASSIFICATION:
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us-09-826-7914-2

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

August 20, 2005, 07:35:07 ; Search time 960 Seconds (without alignments) 176.027 Million cell updates/sec Run on:

Sequence:

US-09-826-791A-2 1712 1 MEPNGTFSNNNSRNCTIENF......KAKTKCVFPVSVWLRKETRV 330 Title: Perfect score:

1612378 seqs, 512079187 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lighting First 45 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Q9ns75 homo sapien	Q95n03 sus scrofa	Q8r528 mus musculu	Q920al mus musculu	Q924t9 rattus norv	ratt	Q95n02 sus scrofa	mus m	homo	homo	Q96p68 homo sapien	Q6y1r5 rattus norv	Q13304 homo sapien	_	_	Q6p852 xenopus tro	P49652 meleagris g		gal	Qenses musculu		-			_	_	P49651 rattus norv	homo	pog	P49650 mus musculu	P32249 homo sapien
SUMMAKIBS		QI	CLT2 HUMAN	CLT2 PIG	Q8R5 <u>2</u> 8	CLT2 MOUSE	CLT2_RAT	CLT1_RAT	CLT1 PIG	CLT1 MOUSE	CLT1 HUMAN	Q81V <u>1</u> 9	GP80_HUMAN	Q6Y1R5	GP17 HUMAN	Q8N5S7	Q7ZZA4	Q6P852	P2YR MELGA	QGIYF8	P2YR_CHICK	Q6NS65	Q9DE05	068907	P2YR_CAVPO	Q90X57	Q7TMV7	P2Y5 CHICK	P2YR RAT	P2YR_HUMAN	P2YR_BOVIN	P2YR MOUSE	EBI2_HUMAN
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		Score	1712.	1367.5	1204	1197	1187	567.5	563	260	559	553	487.5	479	479	477	477	473.5	470	468	467	459	457	456	454	453	449.5	447	447	446	442	442	440
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Q8bmj5 mus musculu P41657 homo sapien Q7230 homo sapien Q8bmc0 mus musculu P41211 homo sapien Q7236 homo sapien Q7236 homo sapien Q89677 homo sapien Q8bki mus musculu Q5kKi mus musculu Q5kKi mus musculu Q8h1232 rattus norv Q8big2 mus musculu P35383 mus musculu P21556 cavia porce
QBBMJ5 P2Y5 HUMAN P2Y5 HUMAN P2Y350 P2Y2 MOUSE P2Y2 HUMAN Q6N356 P2Y9 HUMAN Q6NSP5 QBBKK1 Q8BKK1 Q8BKK1 Q8BKZ1 Q8BKZ1 P2Y2 MOUSE P2Y2 MOUSE P2Y2 MOUSE
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ALIGNMENTS

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SEQUENCE FROM N.A.

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61 MINIAISDILFISTIPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
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Cytoplasmic (Potential).
By similarity.
N-linked (GlcNAc...) (Potential)
N-linked (GlcNAc...) (Potential)
                                                                                                         Extracellular (Potential).
1 (Potential).
Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS00237; G PROTEIN RECEP_F1_1; FALSE_NEG.

PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

G-protein coupled receptor; Glycoprofein; Transmembrane.

DOMAIN

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43

63

1 (Potential).
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; EB54A4A2DDCESEE4 CRC64;
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Extracellular (Potential).
5 (Potential).
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100.0%; Pred. No. 5.9e-99;
tive 0; Mismatches 0;
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Eukaryota; Metazoa; Chordata;
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                                                             RR SEQUENCE FROM N.A.

RA Abdroff K.W., Barren J., Ashurst J.L., Howe K.L.,

RA Abdroff K.J., Barren J., Ashurst J.L., Howe K.L.,

RA Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K.

RA Ainscough R., Almeida J.P., Ambrose K.D., Andrews D.T.,

RA Ainscough R., Barten B.W., Bargulay C.L., Bailey J., Bannerjee R.,

RA Ainscough R., Bartes M.K., Baggulay C.L., Bailey J., Bannerjee R.,

RA Barlow K.F., Bartes K., Bassley H., Erader C., Carter N.P.,

RA Barlow K.F., Bartes R., Barsley H., Clarke G., Clee C.M.,

RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,

RA Clegg S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,

RA Clegg S.C., Garnett J., Glibert J.G., Hall R.E., Hammond S.,

RA Blington A.G., Faulkner L., Frankish A.G., Frankland J., French L.,

RA Garner P., Garnett J., Glibert J.G.R., Gilson C.J., Hanmond S.,

RA Hurley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,

RA Hurley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,

RA Hurle P.J., Hurl A.R., Johnson C., Leongamornlert D.A.,

RA Hurle P.J., Muckerson T., Palmer S.A., Pearce A.V., Peck R.J.,

RA Mashreghi-Mohammadi M., McLaren S.J., McMirray A., Milne S.,

Rock M.J.F., Nickerson T., Palmer S.A., Pearce A.V., Peak R. Shownkeen R., Shownkeen R., Showner C., Shownkeen R., Tracey A., Tromans A., Tubby B.,

Rall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L., Wary D.W., Whitehead S.L., Williang L., Wary D.W., Wright M.W., Young L., Coulson A., Durbin R.,

Rall M., Wallis J.M., West A.P., Whitehead S.L., Willey D., Wary M. M., Riber B.,

Rall M., Wallis J.M., West A.P., Warten S., Bentley D.R., Rogers J., Ross M.T.;

Ralling L., Wary D.W., Wright M.W., Young L., Coulson A., Durbin R.,

Ralling L., Wary D., West A.P., Warten S., Bentley D.R., Rogers J., Ross M.T.;

Ralling L., Wary D., Walley M., Walley S.,

Ralling M. R., Showner R. W., Showner R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Homo sapiens cysteinyl leukotriene receptor 1 like receptor.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. Stimulation by BAY u9773, a partial agonist, induces specific contractions of pulmonary veins and might also have an indirect role in the relaxation of the pulmonary vascular endothelium. The rank order of affinities for the leukotrienes is InC4 = LTD4 >> LTD4.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- TISSUE SPECIFICITY: Widely expressed, with highest levels in the heart, placenta, spleen, peripheral blood leukocytes and adrenal gland. In lung, expressed in the interstitial macrophages, and slightly in smooth muscle cells.

-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
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BMBL, AF254664; AAG17281.1; --
EMBL, AF279611; AAK69485.1; --
EMBL, AB083603; BAB89316.1; --
EMBL, AT385904; AAQ9130.1; --
EMBL, AL131118; CAC29102.1; --
EMBL, AB041644; BAB16379.1; --
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Suga H.;

136

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Length 346;

(Potential) (Potential)

SEQUENCE FROM N.A. Ranaski J., Mateumoto M., Mateumoto S., Saito T., Rambhara M., Takasaki J., Mateushime H., Furnichi K.; Obishi T., Soga T., Mateushime H., Furnichi K.; Characterization of the cloned rat and porcine cysteinyl leukotriene Eukaryota; Metázoa, Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Name-CYSLTR2; Synonyms-CYSLT2; KSALRKGHPQKAKTKCVFPVSVWLRKETRV 330 Ş 345 AC DATE OF THE PRINCE OF THE P

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CLT2 MOUSE
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ID _CLT2_M
AC Q920A1
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DT 28-FEB
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                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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            mitted (bEC-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Receptor for cysteinyl leukotrienes. The response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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4 (Potential).
Extracellular (Potential)
5 (Potential).
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N-linked (GlcNAc. . .)
N-linked (GlcNAc. . .)
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InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=22013942; PubMed=11854273; DOI=10.1074/jbc.M109447200;
MEDLINE=22013942; PubMed=11854273; DOI=10.1074/jbc.M109447200;
Ogasawar H., Ishii S., Yokomizo T., Kakinuma T., Komine M.,
Tamaki K., Shimizu T., Izumi T.;
"Characterization of Mouse Cysteinyl Leukotriene Receptors mCysLT1 and
mCysLT2. DIFFERENTIAL PHARMACOLOGICAL PROPERTIES AND TISSUE
DISTRIBUTION.";
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 277:18763-18768 (2002).

EMBL, AB058930; BAB6681.1; -.

MGD, MG1:191739; Cysltr2.

GO, GO:0016021; C:integral to membrane; TAS.

GO; GO:001631; F:cysteinyl leukotriene receptor activity; IDA.

InterPro; IPR004071; Cysleuk_receptor.

InterPro; IPR000276; GPCR_Rhodpsn.
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                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.3%; Score 1204; DB 2;
Best Local Similarity 73.4%; Pred. No. 2e-67;
Matches 226; Conservative 30; Mismatches 52;
317 LKSALRKGRPQ--KTRCGFSVCVWLKKETRV 345
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(Rel. 41, Last sequence update)
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                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                 Name=Cysltr2;
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                                                                                                                                                                             Hui Y., Yang G., Galczenski H., Figueroa D.J., Austin C.P.,
A Copeland N.G. Gilbert D.J., Jenkins N.A., Funk C.D.;
The mutine cysteinyl leukotrises 2 (CysLT2) receptor. CDN and
The mutine cysteinyl leukotrises 2 (CysLT2) receptor. CDN and
The mutine cysteinyl leukotrises 2 (CysLT2) receptor. CDN and
T genomic cloning, alternative splicing, and in vitro

T characterization.";
D.J. Biol. Chem. 276:47498949495 (2001).

- I. PUNCTION: Receptor for cysteinyl leukotrises. The response is
mediated via a G-protein that activates a phosphatidylinositol-
calcium second messenger system. The rank order of affinities for
the leukotrienes is LTC4 = LTD4.

- SUBCELLULAR LOCATION: Integral membrane protein.

- IISSUE SPECIFICITY: Widely expressed at low levels, with highest
expression in the spleen, thymus and adrenal gland, and lower in
the kidney, brain and peripheral blood leukocytes.

- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1917336; Cysltr2.
MGD; MGI:1917336; Cysltr2.
GO; GO:0016020; C:membrane; IDA.
GO; GO:0001631; F:cysteinyl leukotriene receptor activity; IDA.
InterPro; IPR004071; Cysleuk receptor.
InterPro; IPR00276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -linked (GlcNAc. . .) (Potential) 327B14A6EDDD2A02 CRC64;
                                                                                                                                                                    MEDLINE=21601669; PubMed=11591709; DOI=10.1074/jbc.M107556200;
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2 (Potential).
Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
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PROSITE; PS50262; GPROTEIN RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprofein; Transmembrane.
DOMAIN 26

Extracellular (Potential).
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Extracellular (Potential).
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Extracellular (Potential).
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25-OCT-2004 (Rel. 45, Last annotation update)
Cystainyl leukotritene receptor 2 (CysLTR2).
Name-Cysltr2; Synonyms-Cyslt2;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity.
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35227 MW;
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                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                NCBI_TaxID=10090;
                                                                                                                                                    TISSUE=Heart;
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                                                                                                                                                                             181 SLLIMNHIAVAVGFLLPFLTLTVCYLLIIRILLKABIPESGPRAAHRKALTTIVIAMITF 240
MINLAISDILFISTIPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVR 120
                            61 MENLATSDFLFISTLPPRADYYFRGSNWIFGDLACRVMSYSLYVNMYTSIYFLTVLSVVR 120
                                                                             FLAMVHPFRLLHVTSIRSAWILCGIIWILIMASSIMLLDSGSEQNGSVTSCLELNLYKIA 180
                                                                                                                121 FQATVHPFRMFHVTSVRSAWILCGIIWVFIMASSALLLVNGQEEKDNIISCLELSPOKFK 180
                                                                                                                                                                                                                                    241 FLCFLPYHTLRTVHLTTWKVGLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRL 300
                                                                                                                                                                                                                                                         241 LLCFLPYHALRTLHLVTWDKDSCGDVLHKATVITLTMAAANSCFNPFLYYFAGENFKARL 300
                                                                                                                                                         181 KLOTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Katsaki J., Matsumoto M., Matsumoto S., Saito T., Kambhara M., Takasaki J., Matsumoto M., Matsumoto M., Soya T., Matsushime H., Furuichi K.; "Characterization of the cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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Pfam; PF00001; 7tm 1; 1.

PRINTS; PR01533; CYSTRECPTR.

PRINTS; PR01533; GPCRHODOPSN.

PROSITE; PS00237; GPRCTEIN RECEP F1_1; FALSE_NEG.

PROSITE; PS50262; G PROTEIN RECEP F1_2; 1.

G-protein coupled receptor; Glycoprotein; Transmembrane.

A7 1 (Potential).
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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2 (Potential).
Extracellular (Potential).
3 (Potential).
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28-FEB-2003 (Rel. 41, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Cysteinyl leukotriene receptor 2 (Cysternyl leukotriene receptor 2 (Cysternyl Synonyms=Cyslt2;
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Cytoplasmic (Potential).
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InterPro; IPR000276; GPCR_Rhodpsn.
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53; Indels

31; Mismatches

Best Local Similarity '2.' Matches 224; Conservative 09

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There are no restrictions on
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Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential)
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Extracellular (Potential)
7 (Potential).
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Local Similarity 36.7%; Pred. No. 7.8e-28;
es 122; Conservative 70; Mismatches 115;
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                                       send an email to license@isb-sib.ch).
 European Bioinformatics Institute.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
   4 (Potential).

S. (Potential).

(Ytoplasmic (Potential).

6 (Potential).

Extracellular (Potential).

7 (Potential).

Cytoplasmic (Potential).

By similarity.

N-linked (GlCNNc. .) (Potential).

N-linked (GlCNNc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S., Ohishi T., Soga T., Matsushime H., Furuichi K.; "Characterization of cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                               ö
                                                                                                                                          69.3%; Score 1187; DB 1; Length 309; 73.1%; Pred. No. 2.3e-66;
                                                                                                                                                               57; Indels
                                                                                                                      A122AC8177879D56 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Cysteinyl leukotriene receptor 1 (CysLTR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 AA
                                                                                                                                                               26; Mismatches
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                                                                                                                      35507 MW;
                                                                                                                                                               Conservative
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309 AA;
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225; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 SFMPYHIQRAIHLHFLHSETRSCDSVLRMQKSVVITLSLAASNCCFDFLLYFFSGGNFRR 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISDLIFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 HPFRLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--L 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 CFLPYHTLRTVHL--TTWKVGLCKD--RLHKALVITLALAAANACFNPLLYYFAGENFKD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 TFSNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 QTMNYIALVVGCLLPPFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By similarity.

N-linked (GlcNAc. . ) (Potential)
N-linked (GlcNAc. . ) (Potential)
281B41DF050DF9BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 339;
                                                                                                                                                                                                                                                                               DR RGD; 619796; Cyslt.r.

BR InterPro; IPR000276; GPCR_Rhodpsn.

DR Fam; PR000177 (Cysleuk receptor.

DR PERM; PR000177 (The 1; 1.

DR PERM; PR000177 (Tysl.recptr.)

R PR051TE; PR00237; GPCRRHODOPSN.

R PR051TE; PS00237; GPROTEIN RECEP F1 1; FALSE_NEG.

R PR051TE; PS00237; GPROTEIN RECEP F1 1; FALSE_NEG.

R PR051TE; PS00237; GPROTEIN RECEP F1 2; 1.

R DOMAIN 30 Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extracellular (Potential).
1 (Potential).
Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
3 (Potential).
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SEO MPYHIQRITHLHF----LHNDTKHCDSVLRMQKSVXITLSLAASNCCFDPLLYFFSGGNF 305
132 VQNINLITHKKAKIVCIAIWIFVILTSSPFLMSTSYKDEKNNTKCFEPPQXNQAKYHVLV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/Sv;
PubMed=11226226; DOI=10.1073/pnas.041624398;
Maekawa A., Kanaoka Y., Lam B.K., Austen K.F.;
Maetawa A., Kanaoka Y., Lum B.K., Austen K.F.;
"Identification in mice of two isoforms of the cysteinyl leukotriene 1
receptor that result from alternative splicing.";
Proc. Natl. Acad. Sci. U.S.A. 98:2256-2261(2001).
                                            MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCF
                                                                      245 LPYHTLRTVHLTTWKVGLCKD-----RLHKALVITLALAAANACFNPLLYYFAGENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN-CZECH II; TISSUB-Mammary gland;
STRAIN-CZECH II; TISSUB-Mammary gland;
MEDLINE-22388257; Pubmed-12477932; DDI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshhyuki S., Carninci P., Prange C.,
Brownstein M.J., Deters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
STRANBECFBL/6; TISOSEDE=Trachea;
MEDLINB=2156232; PubMed=11705452; DOI=10.1016/S0006-2952(01)00774-2;
Martin V., Sawyer N., Stocco R., Unett D., Lerner M.R., Abramovitz M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21240338; PubMed=11342226; DOI=10.1016/S0167-4781(00)00271-2; Mollerup J., Jorgensen S.T., Hougaard C., Hoffmann E.K.; "Identification of a murine cysteinyl leukotriene receptor by expression in Xenopus laevis Oocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D4
                                                                                                                                                                                                                                                                                                                                                                                                       Q99JR4; Q9JJ71; Q9JK47;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Cysteinyl leukotriene receptor 1 (Cysteinyl (Cysteinyl leukotriene receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Molecular cloning and functional characterization of murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=T-cell;
Ogasawara H., Izumi T., Shimizu T.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cysteinyl-leukotriene 1 (CysLT1) receptors.";
Biochem. Pharmacol. 62:1193-1200(2001).
                                                                                                                                                                                                                                                                                                                                                                                    352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression in Xenopus laevis oocytes.";
Biochim. Biophys. Acta 1517:455-459(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Cysitri; Synonyms=Cysiti, Cysitir;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                           297 KDRLKSALRK 306
                                                                                                                                                                                                                                                                     306 REGL-STFRK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Blood
                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Funk
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                                                                                                                                                                              원
                                                                                                                                                                                                                        8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 DLLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFWTAMSFFRCIAIVFP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNNNSRNCTIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAIS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 ASSNTCNDTIDDFRNQVYSTLYSMITVVGFFGNGFVLYVLIKTYHEKSAYQVYMINLAVA 71
                                                                                                                                                                                                                    receptors.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
-1-FUNCTION: Receptor for cysteinyl leukotrienes mediating
constriction of the microvascular smooth muscle during an
inflammatory response. This response is mediated via a G-protein
that activates a phosphatidylinositol-calcium second messenger
system (By similarity) Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                         Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
Ohishi T., Soga T., Matsushime H., Furuichi K.;
"Characterization of cloned rat and porcine cysteinyl leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-linked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.9%; Score 563; DB 1; Length 340; 37.4%; Pred. No. 1.5e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00237; G PROTEIN RECEP F1 1; FALSE NEG.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Glycoprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (Potential).
Cytoplasmic (Potential).
4 (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54F9372A121CE413 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 (Potential).
Cytoplasmic (Potential)
              Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB052686; BAB60826.1; -.
InterPro; IPR004071; Cysleuk_receptor.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 N.
38986 MW;
  Name=CYSLTR1; Synonyms=CYSLT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00001; 7tm 1; 1. -
PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31
52
60
60
1130
1130
1144
1144
1146
1146
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es 116; Conserv
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                    NCBI_TaxID=9823;
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CLT1 HUMAN
AC 09Y271;
DT 28-FEB-
DT 28-FEB-
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BRBL; AF329772; AAK16715.1;

BRBL; AF269303 AAK16716.1;

BRBL; AF269304 AAK16716.1;

BRBL; AF263170; AAF73047.1;

BRBL; AF263170; AAF73047.1;

BRBL; BC027102; AAF73047.1;

BRC; MG1; MG1:1926218; Cysltr1.

GO; GO:00005887; C:integral to plasma membrane; IDA.

GO; GO:000746; P:cell surface receptor activity; IDA.

RCO; GO:000746; P:cell surface receptor linked signal transdu...; IDA.

RITEPPO; IPR000271; Cysleuk receptor.

R InterPro; IPR000276; GPCR_Rhodopsn.

R PFam; PF00001; 77m 1; 1.

R PFAM; PF00001; 77m 1; 1.

R PRINTS; PR01533; GYSLTRECPTR.

R PRINTS; PR01533; GYSLTRECPTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                  Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.M., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-I- FUNCTION: Receptor for cysteinyl leukotrienes mediating construction of the microvascular smooth muscle during an inflammatory response. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

--- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1; Synonyms=Long;

Isoid=0993A4-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microvascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=2; Synonyme=Short; Isode=Original Procession in Isode=O99AA-2; Sequence=VSP 001921; Isode=O99AA-2; Sequence=VSP 001921; Isode=O99AA-2; Sequence=VSP 001921; Isode=O99AA-2; Sequence=VSP 001921; Instance of skin, intermediate levels in the heart, kidney and stomach and lower levels in several other tissues. Isoform 1 is the most abundant form in all tested tissues. Was shown to inhibit eosinophilia, bronchial hyperreactivity and microvascula leakage Zafirlukast (Accolate) and pranlukast (Onon) were also shown to be selective antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PSO0237; G PROTEIN RECEP F1_1; FALSE NEG.
PROSITE; PS50262; G PROTEIN RECEP F1_2; 1.
Alternative splicing; G-proTein coupled receptor; Glycoprotein;
Transmembrane.
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (Potential).
Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential)
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4 (Potential).
Extracellular (Potential)
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247 YHTIRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYPAGENFKDRLKS 302  

247 YHTIRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYPAGENFKRRLS 322  

248 YHIQRTIHLHLHSETRPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRRLS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 LFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
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28-FEB-2003 (Rel. 41, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Cysteinyl leukotriene receptor 1 (CysLJR1) (Cysteinyl leukotriene receptor) (HD4 receptor) (HG55) (HMTWF81).
Name-CYSLTR1; Synonyms-CYSLT1;
HOMO sapiens (Human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                               (Potential). (Potential). (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-leukocyte, Peripheral blood monocytes, and Spleen;
MEDLINE-99393629; PubMed=10462554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.7%; Score 560; DB 1; Length 35
38.5%; Pred. No. 2.3e-27;
ive 69; Mismatches 108; Indels
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SBDC94B3F1CD0CAB CRC64;
                                               7 (Potential).
Cytoplasmic (Potential).
By similarity.
N-linked (GlCNAc. . .) (PN-linked (GlCNAc
                                                                                                                                                                                               | (GlcNAc. ..)
| (GlcNAc. ..)
| (GlcNAc. ..)
| (GlcNAc. ..)
                                                                                                                                                                                                                                                                                                                                                                                               Missing (in isoform 2)
/FTId=VSP 001921.
Y -> D (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                          N-linked (GlcNAc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 38.5
Matches 117; Conservative
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Gequenced by the Guthrie CDNA resource center (www.cdna.org)...;
Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

-- FUNCTION: Receptor for cysteinyl leukortriense mediating
bronchoconstriction of individuals with and without asthma.

Stimulation by LTD4 results in the contraction and proliferation of smooth muscle, deama, eosinophil migration and damage to the mucus layer in the lung. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4

>> LTE4 = LTC4 >> LTB4.

--- SUBCELLULAR LOCATION: Integral membrane protein.

--- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 300201; -. Goods of the state of the st
Foley J.J., Schmidt D.B., Muccitelli R.M., Jenkins O., Murdock P.R., Herrity N.C., Halsey W., Sathe G., Muir A.I., Nuthulaganti P., Dytko G.M., Buckley P.T., Wilson S., Bergema D.J., Hay D.W.P.; "Identification, molecular cloning, expression, and characterization of a cysteinyl leukotriene receptor."; Mol. Pharmacol. 56:657-663(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANDOUS: Selective antagonists, such as montelukast (Singulair), zafirlukast (Accolate) and pranlukast (Onon), are used in the treatment of the asthma crisis.
SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
                                                                                                                                                                                                                                                        Warren C.N., Aronstam R.S., Sharma S.V.; "CDNA clones of human proteins involved in signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inter.
Inter.
Inter.
Inter.
Inter.
Pfan, PF00001; 7tm.1; 1.
Pfan, PF00001; 7tm.1; 1.
PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00337; GPCRHODOPSN.
PROSITE; PS50262; GPROTEIN RECEP. F1.2; 1.
PROSITE; PS50262; GPROTEIN RECEP. F1.2; 1.
Gprotein coupled receptor; Glycoprotein; Transmembrane.
Gprotein coupled receptor; Internation (Potential).
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2 (Potential).
Extracellular (Potential)
3 (Potential).
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Extracellular (Potential)
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Cytoplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
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SEQUENCE FROM N.A.
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ACTIONES-E21388257; Pubbede=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausher R.D., Collins F.S., Wagner L., Sheafer C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
Districtento M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Radyinez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                           128
                                                                                                                                                                                                                                                                                                           70 LLCVCTLPLRVVYYVHKGIWLFGDFLCRLSTYALYVNLYCSIFFMTAMSFFRCIAIVFPV 129
                                                                                                                                                                                                                                                                                                                                                                              189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 PYHIQRTIHLHFLANETKPCDSVLRMQKSVVITLSLAASNCCFDPLLYFFSGGNFRKRL- 306
                                                                                                                                                                                                         68
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                                                                                                                                                                                                                           10 SSATCHDIDDFRNQVYSTLYSMISVVGFFGNGFVLYVLIKTYHKKSAFQVYMINLAVAD
                                                                                                                                                                                                                                                                           69 LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPF
                                                                                                                                                                                                                                                                                                                                             129 RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM
                                                                                                                                                                                                                                                                                                                                                                           130 QNINLVTQKKARFVCVGIWIFVILTSSPFLMAKPQKDEKNNTKCFEPPQDNQTKNHVLVL
                                                                                                                                                                                                                                                                                                                                                                                                               186 NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL
                                                                                                                                                                                                                                                                                                                                                                                                                                  11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD
                                                                                                                                                                         Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                              (GlCNAc. .) (Potential)
(GlCNAc. .) (Potential)
(GlCNAc. .) (Potential)
(GlCNAc. .) (Potential)
                                                                                                                                                                     12;
                                                                                                                                     Length 337;
                                                                                                                                                                     71; Mismatches 106; Indels
                                                                                                     B9B53940F895F245 CRC64;
 Cytoplasmic (Potential).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.
N-linked (GlcNAc.
                                                                                                                                     Score 559; DB 1;
Pred. No. 2.6e-27;
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                                                N-linked
N-linked
N-linked
                                                                                                     38541 MW;
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                                                                                                                                                                     Matches 116; Conservative
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 337
173
6
169
180
262
298
96
169
180
262.
                                                                                                                                                     Similarity
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DOMAIN
DISULFID
CARBOHYD
                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302
                                                   CARBOHYD
                                                                                                     SEQUENCE
                                                                                                                                     Query Match
Best Local
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TRANSMEM
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 RLLHVTSIRSAWILCGIIWI-LIMASSIMLLDSGSEQNGSVTSCLELNLYKIAK--LQTM 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYHTLRTVHLTTW--KVGLCKD--RLHKALVITLALAAANACFNPLLYYFACENFKDRLK 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=21458557; Pubmed=11574155; DOI=10.1016/S0378-1119(01)00651-5;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
"Discovery and mapping of ten novel G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 NSRNC--TIENFKREFFPIVYLIIFFWGVLGNGLSIYVFLQPYKKSTSVNVFMLNLAISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                     Strausberg R.;
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC035750, AAH35750.1;
GO, GO:0016021; Ciintegral to membrane; IEA.
GO; GO:0004974; F:leukotriene receptor activity; IEA.
GO; GO:0004078; F:receptor activity; IEA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR004071; Cysleuk receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      096768; OBGTL1; Created)
10-0CT-2003 (Rel. 42, Created)
11-0CT-2003 (Rel. 42, Last sequence update)
25-0CT-2004 (Rel. 45, Last sequence update)
Probable G protein-coupled receptor GPR80 (P2Y-like nucleotide receptor) (P2Y-1ike GPCR).
Homo gapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                         Length 337;
                                                                                                                                                                                                                                                                                                                                                                                       32.3%; Score 553; DB 2; Length 33 37.7%; Pred. No. 6.2e-27; ive 71; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                   337 AA; 38485 MW; B9B09CE0FD305245 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            337 AA
                                                                                                                                                                                                                                                                                                              PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                     PRINTS; PR01533; CYSLTRECPTR.
PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 275:83-91(2001)
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                   Pfam; PF00001; 7tm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SALRK 306
                                    SEQUENCE FROM N.A.
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                                                         FISSUE=Pancreas;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S., Tsutsumi S., Aburatani H., Asai K., Akiyama Y.; "Genome-wide discovery and analysis of human seven transmembrane helix
                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;
Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
"Identification of G protein-coupled receptor genes from the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Thyroid;
Bruess M., Bonisch H., von Kugelgen I.;
"Molecular cloning and functional characterization of a new human P2Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- FUNCTION: Orphan receptor.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSUE SPECIFICITY: Detected in kidney and, to a lower extend, i placenta. Not detected in brain tissues including the frontal cortex, caudate putamen, thalamus, hypothalamus, hippocampus or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the G-protein coupled receptor 1 family
                                                                          nek
Wittenberger T., Hellebrand S., Munck A., Kreienkamp H.-J., Schaller H.C., Hampe W.; "GRPSP, a new G protein-coupled receptor with homology to a subgroup of nucleotide receptors."; BMC Genomics 3:17-17(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00001; 7tm_1; 1.

RRINTS; PR00237; GFCRHODOPSN.

RROSITE; PS0227; GFROTEIN RECEP_F1_1; FALSE_NEG.

RROSITE; PS0226; G FROTEIN RECEP_F1_2; 1.

M G-protein coupled receptor; Glycoprotein; Transmembrane.

T DOMAIN 134 EXTRACellular (Potential).

T TRANSMEM 35 51 (Potential).

T TRANSMEM 56 69 Cytoplasmic (Potential).

T TRANSMEM 50 90 2 (Potential).

FT TRANSMEM 117 137 3 (Potential).

FT TRANSMEM 117 137 3 (Potential).

FT TRANSMEM 117 137 4 (Potential).

FT DOMAIN 138 151 Cytoplasmic (Potential).

FT TRANSMEM 152 172 4 (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor genes.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extracellular (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR002286; P2_purnocptor.
Pfam; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome sequence.";
FEBS Lett. 520:97-101(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:4531; GPR80.
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69
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HUMAN
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                                                                                                                                                                                              LLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNWYSSIYFLTVLSVVRFLAMVHPF 128
                                                                                                                                                                                                           140 SCFSIHKTRCAVVACAVVWIISLVAVIPMTFLITSTNRTNRSACLDLITSDELNIIK--- 196
                                                                                                                                                                                                                                          129 RLLHVTSIRSAWILCGIIWILIMASSI----MLLDSGSEQNGS----VTSCLELNLYKIAK 181
                                                                                                                                                                                                                                                                                       182 LQTMNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFF 241
                                                                                                                                                                                                                                                                                                             --WYNLILTATTFCLPLVIVTLCÝTTIIHTLTHGLQTDSCLK---QKÁRRLTÍLLLLAFY 251
                                                                                                                                                                                                                                                                                                                                  LCFLPYHTLRTVHLTTWKVGL---CKDRLHKALVITLALAAANACFNPLLYYFAGENFKD 298
                                                                                                                                                                                                                                                                                                                                                 79
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                                                                                                                                                             14 NCTIEN--FKREFFPIVYLIIFFWGVLGNG--LSIYVF-LQPYKKSTSVNVFMLNLAISD
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C STRAIN-Sprague-Dawley;
X PubMed=15001573; DOI=10.1074/jbc.M400360200;
R Inbe H., Watcanabe S., Miyawaki M., Tanabe B., Encinas J.A.;
Inbe H., Watcanabe S., Miyawaki M., Tanabe B., Encinas J.A.;
In Identification and Characterization of a Cell-Surface Receptor,
P2Y15, for AMP and Adenosine.";
J. Biol. Chem. 29:18790-19799(2004).
R BMBL; AY191367; AAP32736.1;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0045028; F:purinergic nucleotide receptor activity, G-...;
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:rhodopsin-like receptor activity; IEA.
GO; GO:0007186; P:rhodopsin-like receptor activity; IEA.
InterPro; IPR00276; GPCR_Rhodpsn.
InterPro; IPR00276; GPCR_Rhodpsn.
InterPro; IPR00276; GPCR_Rhodpsn.
           (Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                            29;
                                                                                                    28.5%; Score 487.5; DB 1; Length 337; 34.9%; Pred. No. 7.3e-23; ive 64; Mismatches 114; Indels 29.
                                                                                6814EA0044756CE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 AA; 38377 MW; 9899E80DE0531CB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
G protein-coupled receptor 80.
By similarity.
N-linked (GlCNAc. .
N-linked (GlCNAc. .
N-linked (GlCNAc. .
N-linked (GlCNAc. .
F - L (in Ref. 5) .
K -> R (in Ref. 5) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00217; GPCRHODOPSN.
PRINTS; PR01157; P2YPURNOCPTR.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                              312 AVCSTVRCKVSGNLEQAK 329
                                                                                                                                                                                                                                                                                                                                                                                 RLKSALR---KGHPOKAK 313
                                                                                38251 MW;
                                                                                                               Best Local Similarity 34.9
Matches 111, Conservative
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 183
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176
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236
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 106
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SEQUENCE
         CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                 80 LLYLTSLPFLIHYYASGENWIFGDFMCKPIRFGFHFNLYSSILFLTCFSLFRYIVIHPM 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                     129 RLLHVTSIRSAWILCGIIWILIMASSI----MLLDSGSEQNGSVTSCLEL-NLYKIAKLQT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          245 LPYHTLRTVHLTTWKVGL---CKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRLK 301
                                                                                                                                                 68
                                                                                                                                                                                                                 79
                                                                                                                                                                                                                 23 NCTDEQISFKMQYLPVIYSIIFLVGFPGNTVAISIYVFKMRPWKSST---IIMLNLALTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 YNLILTATTFCLPLLIVTLCYTTIISTLTHGPRTHSCFK---QKARRLTILLLLVFYVCF
                                                                                                                                             14 NCTIE--NFKREFFPIVYLIIFFWGVLGN--GLSIYVF-LOPYKKSTSVNVFMLNLAISD
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MEDLINE-98181695; PubMed-9523551;
Blaesius R.H., Weber R.G., Lichter P., Ogilvie A.;
"A novel orphan G protein-coupled receptor primarily expressed in the brain is localized on human chromosomal band 2q21.";
J. Neurochem. 70:1357-1365(1998).
-: FUNCTION: Putative receptor for purines coupled to G-proteins (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 MNYIALVVGCLLPFFTLSICYLLIIRVLLKVEVPESGLRVSHRKALTTIITLIIFFLCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Raport C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B., Godiska R., Gray P.W.;
"New members of the chemokine receptor gene family.";
                                                                          Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                          20;
       Length 337;
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01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Probable P2Y purinoceptor GPR17 (P2Y-like receptor) (R12)
Name-GPR17;
Ouery Match 28.0%; Score 479; DB 2; Length 33
Best Local Similarity 34.2%; Pred. No. 2.4e-22;
Matches 104; Conservative 66; Mismatches 114; Indels
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-:- SUGCELLULAR LOCATION: Integral membrane protein
-:- AITERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q13304-1; Sequence=Displayed;
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SAVR 318
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TISSUE=Brain;
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                             RESULT 14
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        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 HPVKSLKLRRPLYAHLACAFLWVVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 HALVSLAVAFTFPFITTVTCYLLIIRSL-----RQGLRVEKRLKTKAVRMIAIVLAIFL 273
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                                                                                                                                                                                                                                                                                                                                                                                          By similarity.
N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
                                                                                                                          GO; GO:0005897; C:integral to plasma membrane; TAS.
GO; GO:0004950; F:chemokine receptor activity; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin.
InterPro; IPR00226; GPCR. Rhodpsn.
InterPro; IPR002286; P2_purnocptor.
                                                                                                                                                                                     PRINTS; PRO0237; GPCRHODOPSN.
PROSITE; PS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
Alternative splicing; G-protein coupled receptor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 1; Length 367; 2.6e-22;
 institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Pred. No. 2.6e-22;
62; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                    s (Potential).
Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
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5 (Potential).
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132FBE97BE83C60C CRC64;
                                                                                                                                                                                                                                                         Cytoplasmic (Potential).
2 (Potential).
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Missing (in isoform 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     40989 MW;
                                               EMBL; U33447; AAB16746.1; -. EMBL; Y12546; CAA73144.1; -.
                                                          EMBL; Y12546; CAA73144.1; -. EMBL; Z94154; CAB08107.1; -. EMBL; Z94155; CAB08108.1; -. HSSP; P34996; IDDD.
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nes 112; Conservative
                                                                                               Genew; HGNC:4471; GPR17.
H-InvDB; HIX0002439; -
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TELENBE-2238825; Pubbmed=12477932; DOI=10.1073/pnas.242603899;

A Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A pletchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bacheton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., WcKernan K.J., Male Y.J., Gunarane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Ficher J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutferfield G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Gones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 ISDLLFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 VADLSCVLVLPTRLVYHFSGNHWPFGELACRLTGFLFYLNMYASIYFLTCISADRFLAIV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 HPFRLLHVTSIRSAWILCGIIWILI-MASSIMLDSGSEQNGSVTSCLELNLYKIAKLQT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     || : | : | : | : | : | : | : | : | 191

135 HPVKSLKLRRPLYAHLACAFLWVVAVAMAPLLVSPQTVQTNHTVVCLQ--LYR-EKASH 191
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                                                                                                                                                                                                                                                                                                                                                                                                          Homo sápiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031653; AAH31653.1; -.
GO; GO:00165021; C:integral to membrane; IEA.
GO; GO:0045028; F:urhodopsin-like receptor activity, G-.
GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
GO; GO:000186; P:G-protein coupled receptor protein signalin.
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PRINTS, PRO1157, PZYPURNOCPTR.

PROSITE, PS00237, G PROTEIN RECEP F1 1, UNKNOWN 1.

PROSITE, PS00262, G PROTEIN RECEP F1 2; 1.

SEQUENCE 339 AA, 37860 MW, BB0CAFD0FC371D63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                     339
                                                                                                                                                                                                                                                                Created)
334 HALCNLLCGKRLKGPPPSFEGK 355
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InterPro, IPR002286, P2_purnocptor.
                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ведпенсев.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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192 HALVSLAVAFTFPFITTVTCYLLIRSL-----RQGLRVEKRLKTKAVRMIAIVLAIFL 245
                                                                                                                                                                                 346 VCFVPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFR 305
185 MNYIALVVGCLLPPFTLSICYLLIIRVLLKVEVPESGLRVSHR---KALTTIITLIIFF 241
                                                                                                                                         242 LCFLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAAANACFNPLLYYFAGENFK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 LFISTLPFRADYYLRGSNWIFGDLACRIMSYSLYVNMYSSIYFLTVLSVVRFLAMVHPFR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 IALVVGCLLPFFTLSICYLLIRVLLKVEVPESGL----RVSHRKALTTIJITLIFFL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CFLPYHTLRTVHLTTWKV--GLCK--DRLHKALVITLALAAANACFNPLLYYFAGENFKD 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 SCTFDEEFKYILLPVSYSLVCFFGLILNSVALMMFITKARPWKPST---VYMFHLALSDT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 NCTI-ENFKREFFPIVYLIIFFWGVLGNGLSIYVF---LQPYKKSTSVNVFMLNLAISDL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 26, Last annotation update)
SI:bZ46J2.9 (Novel protein similar to nucleotide receptors).
Name=pr2941; Synonyms=SI:bZ46J2.9, slc2bas;
Brachydanio rerio (Zebzafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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ZFIN; ZDB-GENE-030616-77; pr2y41.
ZG) GO:001621; Cintegral to membrane; IEA.
GO; GO:0016229; F:purinergic nucleotide receptor activity, G-.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000184; F:rhodopsin-like receptor activity; IEA.
GO; GO:000188; F:rhodopsin-like receptor protein signalin.
InterPro; IPR00018; P2Y4_purnocptor.
InterPro; IPR00018; P2Y4_purnocptor.
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81; Mismatches 111; Indels
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR01056; P2Y4PRNOCPTR.
PRINTS; PR01157; P2YPURNOCPTR.
PROSITE; PR00237; G PROTEIN RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 AA
                                                                                                                                                                                                                                                                               298 DRLKSAL----RKGHPQKAKTK 315
                                                                                                                                                                                                                                                                                                                                                306 HALCNLLCGKRLKGPPPSFEGK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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072ZA4
1D Q7ZZA4
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OM nucleic - nucleic search, using sw model

August 20, 2005, 04:45:55; Search time 213 Seconds (without alignments) 7628.276 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-826-791A-1 993 1 atggaaccaaatggcacctt.....gaaaggaaacaagagtataa 993

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1202784 seqs, 818138359 residues Searched:

2405568 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Database

sued(Patent) NA:*
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/cgn2_6/ptodata/1/ina/RB_COMB.seq:*
/cgn2_6/ptodata/1/ina/RB_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	31,	148		43,	43,	43,	۲,	183	e,	Sequence 3, Appli	۳,	'n	۳,	'n	Sequence 1, Appli	62,	62,	62,	62,	62,	16,	16,	ı,	٦,
SUMMARIES		σī	US-09-585-876-1	US-09-044-404A-1	US-09-586-924-1	US-09-170-496D-31	US-09-016-434-1484	US-08-153-848-43	US-09-299-843A-43	US-09-088-337B-43	PCT-US93-11153-43	PCT-US95-07180-1	US-09-170-496D-181	US-08-097-938-3	US-08-476-000-3	US-08-472-840-3	US-08-476-976-3	US-08-474-410-3	US-08-486-673B-3	US-08-742-440A-1	US-08-476-000-62	US-08-472-840-62	US-08-476-976-62	US-08-474-410-62	US-08-486-673B-62	US-08-889-108-16	PCT-US94-10358-16	US-08-454-549-1	US-08-454-552-1
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de	Query	Matc	(49.7))	14.6	10.0	10.0	10.0	10.0	10.0	10.0	10.0	7.6	9.3	9.3	9.3	9.3	9.3	9.3	9.1	9.1	9.1	9.1	9.1	9.1	9.8	9.8	9.8	9.6
		Score	989.8	145.2	145.2	99.4	99.4	99.4	99.4	99.4	99.4	99.4	96.2	92	92	92	92	92	92	90	90	90	90	90	90	85.6	92.6	85.6	85.6
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ALIGNMENTS

RESULT 1 US-09-581-876-1 US-09-581-876-1 US-09-581-876-1 US-09-581-876-1 US-09-581-876-1 US-09-581-876-1 US-09-581-871-00 US-09-581-1 US-08-871-1 US-08-881-1 US-0	Query Match 99.7%; Score 989.8; DB 4; Length 1401; Best Local Similarity 99.8%; Pred. No. 8.2e-307; Indels 0; Gaps 0; Matches 991; Conservative 0; Mismatches 2; Indels 0; Gaps 0; N 1 ATGGAACCAAATGGCACTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTC 0 Gaps 0; Gaps 0;	b 425 ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGCTGAC 484
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1114 ACTAAAAAATCAATGAAAAAAATCTGTCAAG-----TCATAAAAAGGCTATAGGAAT 1167
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Pred. No. 1.1e-35;
0; Mismatches 398;
     7.0
 SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,404A
FILING DATE: MARCH 19, 1998
CLASSIFICATION: 435
                                                                                                                                                                                                                 GH-70001-1
                                                       FILING DATE: MARCH 19, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/844,795
FILING DATE: APRIL 22, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T.
                                                                                                                                                                                       REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH 1578 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 14.6%; al Similarity 51.5%; 451; Conservative
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TELEX:
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Best Local Similarity
Matches 451; Conservat
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ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
APPLICANT: ELLIS, CATHERINE
APPLICANT: AMES, ROBERT
APPLICANT: SOLEY, JAMES
APPLICANT: SARAU, HENRY
TITLE OF INVENTION: CDNA CLONE HMIMF81 THAT ENCODES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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0 Swedeland Road, P.O. Box 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09044404A
Patent No. 6200775
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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CITY: King of Prussia
STATE: PA
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US-09-044-404A-1
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APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Chalmers, Derek T.
APPLICANT: Law, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
TITLE OF INVENTION: Receptors
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE PATENTION OF SEQ ID NOS: 294
SEQ ID NO 3: 1
SEQ ID NO 3: 1
LENGTH: 1020
                                                                                                                                                                                                                                                                                                                                                                                1114 ACTAAAAAATCAATGAAAAAAATCTGTCAAG-----TCATAAAAAGGCTATAGGAAT 1167
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                                                       874 ACAGAAAAAAGCCAGGTTTGTGTGTGTAGTATTTGGATTTTTGTGATTTTTGACCAGTTC
                                                                                            AATAATGCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCACATCATGCTTAGAGCT
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                   CATCAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCTT
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Patent No. 6555339
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.8 Matches 339; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: BALLSEY, WENDY
APPLICANT: BALLSEY, WENDY
APPLICANT: BALLS, CATHERINE B.
APPLICANT: FOLEY, JAMES, ROBERT S.
APPLICANT: AREAU, HENRY M.
APPLICANT: CHAMBERS, JON
TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
FILE REPERENCE: GH-70001-1D1
CURRENT APPLICATION WHOMBER: US/09/S86,924
CURRENT FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: 09/044,404
PRIOR APPLICATION NUMBER: 08/844,795
PRIOR APPLICATION NUMBER: 08/844,795
NUMBER OF SEQ ID NOS: 2
NUMBER OF SEQ ID NOS: 2
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTESO for Windows Version 3.0
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                                                                                                                                                                                                                                                                     864 CIATTACTTTGCTGGGAGAATTTTAAGGACAGACT 899
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09586924
Patent No. 6506878
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451; Conservative
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Best Local Si
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                                               TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1484:
SEQUENCE CHARACTERIGITCS:
LENGTH: 1900 base pairs
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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Best Local Similarity 48.8%;
Matches 339; Conservative
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STRANDEDNESS: single
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; Patent No. 5759804
; GENERAL INFORMATION:
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; CLONE: 992699
US-09-016-434-1484
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                                                                                                                                                                                                                         CTGGGAACCACTGGCCATTTGGGGGAAATCGCATGCCGTCTCACCGGCTTCCTCTTACC 337
                                                                                                                                                                                                                                                                                                                                                                                                                TGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGGATCCTCTGTG 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     671 ITTCTCACAGGAAGGCACTGACCACCATCATCACCTTGATCATCTTCTTCTTGTGTT 730
218 TGGCCGTGGCCGACTTGTCGTGCGTGCTGGTCCTGCCCACCCGCCTGGTCTACCACTTCT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518 TĠCAGACCAACCACACGGTGGTĊTGCCTGCAGCTGTACCGGGAGAAGGCCTCCCACCATG 577
                                                                                                                                                                                                                                                                                                                                         TCAACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGCGGTTTCCTGGCAA
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Patent No. 6500938
CENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
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NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-09-016-434-1484
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                                                                                                                     1278 CCCTGG-----TGTCCCTGGCAGTGGCCTTCACCTTCCCGTTCATCACCACGGTCACCT 1331
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                                                                       491 AGAACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATAAATTGCTAAGCTGCAGA 550
                                                                                                                                                                        551 CCATGAACTATATTGCCTTGGTGGGCTGCCTGCTGCCATTTTTCACACTCAGCATCT
                                                                                                                                                                                                                                                                                                                                                                       671 TTTCTCACAGGAAGGCACTGACCACCATCATCATCACCTTGATCATCTTCTTCTTGTGTTT
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APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
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FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-UN-1998
PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-299-843A-43
; Sequence 43, Application US/09299843A
; Patent No. 6107475
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jill E. Uhl
REGISTRATION NUMBER: 43,213
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TYPE: nucleic acid
STRANDEDNESS: single
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: Illinois
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APPLICANT: Gray, Patrick W.

PPLICANT: Schweikart, Vicki L.

TITLE OF INVENTION: NO. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bicknell, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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10.0%; Score 99.4; DB 1; Length 1901;
Best Local Similarity 48.8%; Pred. No. 6.1e-21;
Matches 339; Conservative 0; Mismatches 341; Indels 15
                                                                                                                                                                          6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 31794
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-648
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
TYPE: nucleic acid
STRANDENNES: 5: single
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701..1717
                                                                                                                                                 ADDRET: 6300
CITY: Chicago
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; LOCATION:
US-08-153-848-43
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   6300 Sears Tower, 233 South Wacker Drive
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                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
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Pred. No. 6.1e-21;
0; Mismatches 341;
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,3378
FILING DATE: 01-Jun-1998
CLASTION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
                                                                                                                                                                                                                                   COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 701..1717
SEQUENCE DESCRIPTION: SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: NO. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1901 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO: 43:
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Best Local Similarity 48.8%;
Matches 339; Conservative
                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                            CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGGAACCACTGGCCATTTGGGGAAATCGCATGCCGTCTCACCGGCTTCCTCTTCTACC 1037
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Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEGURNCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                          Length 1901;
                                                                                                                                                                                                                                   Score 99.4; DB 3; Length 19 Pred. No. 6.1e-21; 0; Mismatches 341; Indels
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                                      (genomic)
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                                                                                                                                                                                                                            Query Match
Best Local Similarity 48.8
Matches 339; Conservative
                                                                                                                                     7171..107
TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                           ), NAME/KEY:

), LOCATION:

US-09-299-843A-43
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US-09-088-337B-43
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GENERAL INFORMATION:
APPLICANT: L1, YI
APPLICANT: GOCAYNE, JEANINE D
APPLICANT: GOCAYNE, JEANINE D
APPLICANT: GOCAYNE, JEANINE D
TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
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CITY: ROSELAND
STATE: NJ
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APPLICANT: Gray, Patrick W.
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAtentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153 FILING DATE: PCT/US93/11153 FILING DATE: PCT/US93/11153 FILING DATE: PROPLICATION NUMBER: US 07/977,452 FILING DATE: 17-NOV-1992 ATTONEY/AGENT INPORMATION: NUMBER: US 07/977,452 FILING DATE: 17-NOV-1992 ATTONEY/AGENT INPORMATION:
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GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity 48.8
Matches 339; Conservative
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STATE: Illinois
COUNTRY: HEA
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10.0%; Score 99.4; DB 5; Length 24
Best Local Similarity 48.8%; Pred. No. 7.2e-21;
Matches 339; Conservative 0; Mismatches 341; Indels
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              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 201-994-1740
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2453 base pairs
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06-JUNE-1995
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STRANDEDNESS: single
TOPOLOGY: linear
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548..1564
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; LOCATION:
PCT-US95-07180-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 343;
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Pred. No. 4.4e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               731 TCCTGCCCTATCACACACTGAGGACCGTCCACTTG 765
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Sequence 181, Application US/09170496D Patent No. 6555339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 48.5°
Matches 337; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                       GENERAL INFORMATION:
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APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCAEBOROUGH, ROBERT M.
AITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSE: MORISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CIIY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266 ACTGGAAAACTGACCACTGTCTTCCTTCCAATTGTCTACACAATTGTGTTTTGTGGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 GIGAACGITITCAIGCIAAAICIGGCCAITICAGAICICCIGIICAIAAGCACGCITCCC
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349 AGTGTTGTGCGTTTCCTGGCAATGGTTCACCCCTTTCGGC 388
                                            see adrergeadaderarredercarcergaaceeeragede eos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,000 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/390,301 FILING DATE: 25-JAN-1995 ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: ADLER, REID G.
REGISTRATION NUMBER: 30,988
REFERENCE TUNDER: 2803-0006.20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             Sequence 3, Application US/08476000
Patent No. 5716789
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (202) 887-15-00
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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56
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-08-476-000-3
                                                                                                                                 RESULT 13
US-08-476-000-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             326 ricccaagraacggcarggcccrgrggggrcrrrcrrrrcgaacraagaagaacccr
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9.3%; Score 92; DB 1; Length 1255;
Best Local Similarity 54.4%; Pred. No. 1.1e-18;
Matches 185; Conservative 0; Mismatches 155; Indels
                                                                                                                                                                       APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBORGUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR AND ITS
TITLE OF INVENTION: AGGNISTS AND ANTAGONISTS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE MORRISON & POERSTER
STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,938
FILING DATE: 26-JUL-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURAAHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET UNBER: 29,959
REFERENCE/POCKET UNBER: 29,959
RELEPANCE (202) 897-1500
TELEPAN: (202) 887-0763
                                                                                          Sequence 3, Application US/08097938
Patent No. 5629174
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                          STREET: 2000 Feming. D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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US-08-097-938-3
                                              RESULT 12
US-08-097-938-3
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APPLICANT: SUNDELIN, JOHAN
APPLICANT: SCARBOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
       326 TTGCCAAGTAACGGCATGGCCCTGTGGGTCTTTTCCGAACTAAGAAGAAGCACCCT 385
                                                                                             386 GCTGTGATTTACATGGCCAATCTGGCCTTGGCTGACCTCCTCTCTGTCATCTGGTTCCCC 445
                                                                                                                                            229 TTCAGGGCTGACTATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGG 288
                                                                                                                                                                          506 GIGCTTATTGGCTTTTTCTATGGCAACATGTACTGTTCCATTCTCTTCATGACCTGCCTC 565
                                                   169 GIGAACGITITCAIGCIAAAICIGGCCAITICAGAICICCIGIICAIAAGCACGCIICCC
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Pred. No. 1.1e-18;
0; Mismatches 155; Indels
                                                                                                                                                                                                                                                                                                                         349 AGTGTTGTGCGTTTCCTGGCAATGGTTCACCCCTTTCGGC 388
                                                                                                                                                                                                                                                                                                                                                                   see Adrigigeadaderarisegicaricariseadececarisegic 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS PROPERED FORM:
COMPUTER: PROPERED FORM:
COMPUTER: PROPERED FORM:
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/476,976
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: US 08/390,301
FILING DATE: 25-JAN-1995
ATPOINT MAPPER: 25-JAN-1995
ATPOINT MAPPER: US 08/390,301
FILING DATE: 25-JAN-1995
ATPOINT NUMBER: US 08/390,301
REGISTRATION NUMBER: 30,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 2803-0006.20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08476976
Patent No. 5874400
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(202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1255 base pairs
TYPE: nucleic acid
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Best Local Similarity 54.4
Matches 185; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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56
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LOCATION:
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; LOCATION:
US-08-476-976-3
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                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08472840
Patent No. 5763575
GENERAL INFORMATION:
APPLICANT: SUNDELIN, JOHAN
APPLICANT: SUNDELIN, JOHAN
TITLE OF INVENTION: RECOMBINANT C140 RECEPTOR, ITS AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                         506 GIGCTIATIGGCTITITICIAIGGCAACAIGIACIGITCCATICTCITCAIGACCTGCCTC 565
289 ATTAIGICTIATICCTIGIATGICAACAIGIACAGCAGIATITAITTICCIGACCGIGCIG 348
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0; Mismatches 155; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,840
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STREET: 2000 Pennsylvania Ave. N.W., Ste. 5500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 2803-0006.20
TELECOMMUTCATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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CLASIPECATION: 435
CLASIPECATION DATA:
APPLICATION NUMBER: US/08/390,301
FILING DATE: 25-CAN-1995
ATOMORY/AGENT INFORMATION:
NAME: ADLER, REID G.
REGISTATION NUMBER: 30,909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDUIN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION:
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US-08-472-840-3
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US-08-472-840-3
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Search completed: August 20, 2005, 07:35:01 Job time : 217 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 20, 2005, 04:38:00 ; Search time 3256 Seconds (without alignments) 11608.667 Million cell updates/sec Run on:

US-09-826-791A-1 993 1 atggaaccaaatggcacctt......gaaaggaaacaagagtataa 993 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

34239544 segs, 19032134700 residues Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Lighing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1D COS \$ 21.37 C	CD630068
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439.6	428	414.4	412	404.6	404.4	339.2	333	301.2	179.4	169.2	146.8	143.2	125	123.4	123.4	121	120.4	116.8	116.4	114
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ALIGNMENTS

30842218 N 737 3', mR GI:51323 nns (human) nns Metazoa;	Talking to the property of the	cDNA Libb cDNA Libb DNA Seque Clone dis found that http://im Plate: IR High qual! High qual!	/db_xref="taxon:9606" /clone=!ntaxen:9606" /tissue_type="mixed" /lab_host="DH10B (T1-phage-resistant)" /clone_lib="NIH MGC 146" /note="Vector: pcDNA3.1; Site 1: multiple; Site 2: multiple; ORF's were PCR-amplified (from IMAGE clones or from commercially available cDNA libraries) and cloned by the Guthrite cDNA Resource Center (www.guthrie.org/cDNA) into pcDNA3.1. For specific information on cloning sites (which vary by clone), please refer to the Guthrie website, using the Guthrie ID given in the file
RESULT 1 CO959137/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES BOUTCE	

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                                                                                                                                                                                                                           Query Match 68.0%; Score 675; DB 6; Lv
Best Local Similarity 98.9%; Pred. No. 5.4e-185;
Matches 701; Conservative 0; Mismatches 5;
                                    USA
                                  CA 94304,
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 GCCATTTTTCACACTCCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGCACTGACCACCATCATCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCCCAGAATCGGGGCTGCGGGTTTCTCACAGGAAGGCACTGACCACCATCATCACAC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCACAGAAGGCAAAGAGAAAGTG 947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
ftp://image.llnl.gov.image.rearrayed_plates/IRBF.preSV
a. Note: this is a NIH MGC Library."
                                                                                                                                                  GATTATGTCTTATTCCTTGTATGTCAACATGTACAGCAGTATTATTATTTCTGACCGGGTGCT
                                                                                                                                                                                                            GAGTGTTGCGTTTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCAT
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                                                                                                                                                                                                                                                                                                                                                                                      CTTGATCATCTTCTTGTGTTTCCTGCCCTATCACACTGAGGACCGTCCACTTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACATGGAAAGTGGGTTTATGCAAAGACAGACTGCATAAAGCTTTGGTTATCACACTGGC
                                                                                                                                                                                             GAGTGTTGTGCGTTTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCAT
                                                                                                                                                                                                                                                                                                                          GCTCCTGGACAGTGGCTCTGAGCAGGACGGCAGTGTCACATCATGCTTAGAGCTGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCATTTTTCACACTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGA
                                                                                                                              CAGGAGTGCCTGGATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAAT
                                                                                                                                                                                                                                                                                                                                            GCTCCTGGACAGTGGCTCTGAGCAGAACGGCAGTGTCACATATCATGCTTAGAGCTGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 TAAGGACAGACTAAAGTCTGCACTCAGAAAAGGCCATCCACAGAAGGCCAAAGACAAAGTG
                                                                                                Gaps
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1 (bases 1 to 758)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
                                                                                                .;
                                                               Length 720,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTTTCCCTGTTAGTGTGGTTGAGAAAGGAAACAAGAGTATA 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD630086 758 bp mRNA linear 56040032J1 FLP Homo sapiens CDNA, mRNA sequence. CD630086
                                                                                              0; Indels
                                                           Score 693; DB 7;
Pred. No. 3e-190;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD630086.1 GI:40278352
                                                             69.8%;
llarity 99.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                              Best Local Similarity
Matches 704; Conserv
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                                                                Match
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CD630086
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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EST 12-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AAGAGAGAATTTTTCCCAATTGTATATCTGATAATATTTTTTCTGGGGAGTCTTGGGAAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 Argeraarceroccarrreagarcrecrerrearageaccerrecerreaggereae
                                                                                                                                                                                                                       Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 745)
Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

Circular rapid amplification of cDNA ends for high-throughput
Genomics 84 (1), 205-210 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGAACCAAATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCCTCTGTGGGGATCATAGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 745,
710 ATCGGGCTGCGGGTTTCTCACAGGAAGGCACTGACCACCATCA 753
                                                                                                             linear
                                                                                                           CD630072 745 bp mRNA linee
56039924J1 FLP Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 745
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive Cloning Vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.8%; Score 663; DB 6; I
99.7%; Pred. No. 1.7e-181;
                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                           Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304,
Tel: 6508454102
Email: gfudincyte.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                    CD630072.1 GI:40278338
                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 99.7
Matches 685; Conservative
                                                                                                                                                CD630072
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                                                                                                                           DEFINITION
ACCESSION
VERSION
KEYWORDS
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AUTHORS
TITLE
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COMMENT
                                                                        RESULT 4
CD630072
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AAGAGAGATTTTTCCCAATTGTATATCTGATAATATTTTTTCTGGGGAGTCTTGGGAAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGTTGTCCATATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgeraAarerGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGCTGCAGACCATGAACTATTGCCTTGGTGGTGGCTGCC-TGCTGCCATTTTTCAC 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTA--AAAGTGGAGGT-CCCAGA 656
                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases I to 762)
1 (bases I to 762)
2 (St., Wang, J., Yang, J., Au-Young, J. and Stuve, L.L. Circular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 666; DB 6; Length 762;
Pred. No. 2.38-182;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone lib="Flib"
/note="Vector: pDrive Cloning Vector"
                                                                                                                                                                                                         Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.1%;
Best Local Similarity 99.4%;
Matches 700; Conservative
                                         sapiens
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                                                                          470 ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
                                                                                                                        481 GGCTCTGAGCAGAACGGCAGTGTCACATCATGCTTAGAGCTGAATCTTATAAAATTGCT
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/mol_type="mcN4"
/db_txef="texon:9606"
/clone_lib="Fip"
/note="Vector: pDrive_Cloning_Vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.6%; Score 632; DB 6; Lv
98.3%; Pred. No. 1.8e-172;
live 0; Mismatches 5;
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102.
Email: gfu@incyte.com.
Location/Qualifiers
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Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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                               TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT
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56040096H1 FLP Homo sapiens cDNA, mRNA sequence.
CD630089
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/db_xref="taxon:9606"
/clone_lib="FLP"
/note="Vector: pDrive_Cloning_Vector"
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
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/organism="Homo sapiens"
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Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

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En (Dases I to 673)
En (Gases I to 673)
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

L Genomics 84 (1), 205-210 (2004)
Contact: Pu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfw@incyte.com.
Location/Qualifiers
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1 (Circular rapid amplification of cDNA ends for high-throughput Grecular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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5603996H1 PLP Homo sapiens CDNA, mRNA sequence.
CD630077
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3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102.
Email: gfu@incyte.com.
Location/Qualifiers
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: IRBI7 row: f column: 03

High quality sequence stop: 602.

Location/Qualifiers

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AGENCOURT 30842618 NIH MGC_146 Homo sapiens cDNA clone
IMAGE:7389737 5', mRNA sequence.
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I (bases 1 to 729)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 RM10AO7 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Guthrie CDNA Resource Center
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                                                              Pred. No. 2.1e-168;
                                        Score 618; DB 6;
                                                         100.0%; Pred. No.
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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El (bases 1 to 670)

S. Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes

L. Genomics 84 (1), 205-210 (2004)

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Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102.

Email: gfu@incyte.com.
Location/Qualifiers
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481 GGCTCTGAGCAGAACGGCAGTGTCACATCATGCTTAGAGCTGAATCTCTATAAAATTGCT
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56040088H1 FLP Homo sapiens cDNA, mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone lla="Fth"
/note="Vector: pDrive Cloning Vector"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eu (Bases 1 to 652)
E 1 (Bases 1 to 652)
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
L Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
Incyte Genomics, Inc.
3160 Porter Dr., Palo Alto, CA 94304, USA
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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56040008H1 FLP Homo sapiens cDNA, mRNA sequence.
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llarity 100.0%; Pred. No. 4.9e-164;
Conservative 0; Mismatches 0;
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                                   684
                                                                  706 NNGCTGCGGGTTTCACAAGAAG 729
                                  661 GGGCTGCGGGTTTCTCACAGGAAG
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1 (bases 1 to 68).
1 (bases 1 to 68).
2 (croular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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                                                                                             470 ATCCTCTGTGGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTCGGACAGT
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                      350 TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGGG
                                                                          361 TTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG
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56039908H1 FLP Homo sapiens CDNA, mRNA sequence.
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3160 Porter Dr., Palo Alto, CA 94304, t
Tel: 6508454102
Email: gfu@incyte.com.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone lib="FLP"
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1 (bases 1 to 663)

1 (kases 1 to 663)

Circular rapid amplification of cDNA ends for high-throughput Genomics 84 (1), 205-210 (2004)
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                                  ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
                                                            ATCCTCTGTGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT
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56040016H1 FLP Homo sapiens cDNA, mRNA sequence.
CD630081
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/mol_type="mRNA"
/db_xrefe="taxon:9606"
/clome_lb="Fipp"
/note="Vector: pDrive_Cloning_Vector"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102
Email: gfu@incyte.com.
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clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.lnh.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH MGC Library."
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                                                                                                                                                      Score 565; DB 7;
Pred. No. 6e-153;
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                                                                                                                                                      56.9%; Score 565; DE ilarity 100.0%; Pred. No. 6e-Conservative 0; Mismatches
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3160 Porter Dr., Palo
Tel: 6508454102
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Homo sapiens
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AGENCOURT 14740183 NIH MGC 145 Homo sapiens CDNA clone
IMAGE:6971946 5', mRNA sequence.
CF147785
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/db Xref="taxon:8606"
/db Xref="taxon:8606"
/clone="lnAGE:6971946"
/tissue type="mixed"
/lab_host="DH108"
/clone lib="NHH MGC 145"
/note="vector: pcDNA3.1; Site_l: varies by clone; Site_2: varies by clone; ORPA were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
                                                             360
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-rémail.nih.gov
Tissup Preparation: GPCR Consortium
CDNA Library Preparation: GPCR Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB102 row: f column: 05
High quality sequence stop: 659.
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     ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC 289
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Email: gfu@incyte.com.
Location/Qualifiers
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54.7%; Score 543; DB 6; I
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

August 20, 2005, 02:24:45 ; Search time 4426 Seconds (without alignments) 10871.222 Million cell updates/sec Run on:

OM nucleic - nucleic search, using sw model

US-09-826-791A-1 993 1 atggaaccaaatggcacctt......gaaaggaaacaagagtataa 993 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4708233 seqs, 24227607955 residues Searched:

9416466 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result		Query				
No.	Score	Match	Match Length DB	DB	ΙD	Description
7	993	100.0	993	9	AX304812	AX304812 Sequence
71	993	100.0	993	9	BD131273	BD131273 Novel po]
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ø	993	100.0	1041	9	CQ739544	CQ739544 Sequence
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Patent: JP 2002017378-A 1 22-JAN-2002;
PFIZER INC
OS Homo sapiens (human)
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JP 2002017378-A/1.
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Mammalia; Eutheria;
1 (bases 1 to 993)
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/codon_start="cysteinyl leukotriene receptor like receptor"
/protein_id="BAB16379.1"
/db_xref="cysteinyl leukotriene receptor like receptor"
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Catarrhini; Hominidae; Homo.
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Published Only in DataBase (2000)
2 (bases 1 to 993)
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Submitted (10-fAPR-7009) Hinako Suga, Faculty of Medicine,
University of Tokyo, Department of Neurochemistry, 7-3-1,
Tokyo 113-0033, Japan (E-mail:hsuga@m.u-tokyo.ac.jp,
Tel:81-3-5841-3560, Fax:81-3-3814-8154)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 993)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 1041)

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El (bases 1 to 1041)

El Aga,T., Takeda,S. and Miyake,N.

Novel G-protein coupled receptors

L Patent: JP 2002112793-A 29 16-APR-2002;

JAPAN SCIENCE AND TECHNOLOGY CORP

OS Homo sapiens (human)

PN JP 2002112793-A/29

PD 16-APR-2002

PP 09-FEB-2001 JP 2001034434

PI TATSUYA HAGA, SHIGEKI TAKEDA, NARIKI MIYAKE

PC CLEARS, O9, A01K67/027, A61K38/00, A61K39/395, A61K35/00, PC
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                         CTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCG
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100.0%; Pred. No. 3e-286;
iive 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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JP 2002112793-A/29.
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Location/Qualifiers
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RLHKALVITLALAAANACFNPLLYYFAGGNFKDRLKSALRKGHPQKAKTKCVPPVSVW
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                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                      /note="unnamed protein product"
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/mol_type="unassigned DNA"
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03-FEB 2004

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CQ739544 1041 bp DNA Sequence 25478 from Patent WO02068579.

RESULT 6 CQ739544 LOCUS DEFINITION

Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.

Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
Parent: WO 02068579-A 25478 06-SEP 2002;

PR Corporation (NY) (US) 120 348 360 480 540 648 99 168 180 ATGCTAAATCTGGCCATTTCAGATCTCCTGTTCATAAGCACGCTTCCCTTCAGGGCTGAC 240 288 TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT 300 408 420 468 528 588 900 708 720 768 9 TATTATCTTAGAGGCTCCAATTGGATATTTGGAGACCTGGCCTGCAGGATTATGTCTTAT AAGCTGCAGACCATGAATTGCCTTGGTGGGCTGCCTGCTGCCGCATTTTTCACA TCCTTGTATGTCAACATGTACAGCAGTATTTATTTCCTGACCGTGCTGAGTGTTGTGCGT TICCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG TTCCTGGCAATGGTTCACCCCTTTCGGCTTCTGCATGTCACCAGCATCAGGAGTGCCTGG ATCCTCTGTGGGGATCATATGGATCCTTATCATGGCTTCCTCAATAATGCTCCTGGACAGT GGGTTGTCCATATGTTTTCCTGCAGCCTTATAAGAAGTCCACATCTGTGAACGTTTTC CTCAGCATCTGTTATCTGCTGATCATTCGGGTTCTGTTAAAAGTGGAGGTCCCAGAATCG GGGCTGCGGGTTTCTCACAGGAAGGCACTGACCATCATCATCATCATCATCATCTTC GGGCTGCGGGTTTCTCACAGGAAGGCACTGACCATCATCATCATCATCTTC Homo sapiens (human) Homo sapiens Eukaryots metazoa; Chordata; Craniata; Vertebrata; Butelé Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo ; Length 1041; Indels 'Match 100.0%; Score 993; DB 6; Local Similarity 100.0%; Pred. No. 3e-286; les 993; Conservative 0; Mismatches 0; 1. .1041
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606" Corporation (NY) (US) Location/Qualifiers GI:42342834 709 δ 셤

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Best Local Similarity 100.0%; Pred. No. 3e-286;
Matches 993; Conservative 0; Mismatches 0;
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Patent: WO 0177149-A 118-OCY-2001;)
Bayer Aktiengeeellschaft (DE)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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AX281256 LOCUS DEFINITION ACCESSION RESULT

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Catarrhini, Hominidae, Homo.
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REGENERON PHARMACEUTICALS, INC. (US)
Location/Qualifiers
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Sequence 6 from Patent W00192302.
AX417072 AX417072.1 GI:21449674
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Mammalia; Eutheria; Primates;
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/b xref="G1:1764496"

/db xref="G1:1764496"

/translation="MERKERSLOPSISVSEMEDNGTESNNNSRNCTIENFKREFFPIV
YLITEMSVLGNGE;IYVPLOPYKKGTSVNYFMLNLAISDLLFISTLFPFRADYYLRGS
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IIWILIWASSIYMLLDGGGSEQNGSVTSCLELNIYKIAKLOTMMYIALVVGCLLPFFTLS
ICYLLIIRVLKVEVPESGLRVSHRKALTTIITLIIFFLCFLPYHTLRTVHLTWKV
GLCKDRHKKALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVF
PVSVWLRKETRV"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: BP 1198050-A 5 28-NOV-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)
Location/Qualifiers
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/organism="Homo sapiens" |
/mol type="unassigned DNA" |
/db xref="taxon:9606" |
1. .1041 |
/note="unnamed protein product"
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Sequence 5 from Patent EP1158050.
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PAT 27-FEB-2003
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Patent: WO 02086123-A 29 31-OCT 2002;
Bristol-Myers Squibb Co. (US)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                 AAGTCTGCACTCAGAAAAGGCCATCCACAGAAGGCAAAGACAAAAGTGTGTTTCCCTGTT
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; Pred. No. 3e-286;
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Sequence 29 from Patent WO02086123.
AX644551
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1. _1041
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Whifedlacrims-slynnyssiyer-lanyhperlihtysirabuilce
Ilwillimassiwildbegeegngsvisclelinykiaklotwnyialvvgcllepfflc
Ilwilliwassiwilkvebesgengsvisclelinykiaklotwnyialvvgcllepfflc
Glycliirvlikkluvitalaaanacfnpllyyfagenfkorleythtytwky
Pusywilkkrivitalaaanacfnpllyyfagenfkorleksalrkghpqkaktykyp
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 PI HARLAND LEE
C12N1S/09, A61K39/395, A61K39/395, A61K45/00, A61K48/00, A61P1/04
PC A61P9/00,
PC A61P11/00, A61P11/02, A61P11/06, A61P19/00, A61P23/00, A61P31/00,
PC A61P37/00,
PC C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12NS/10 PC C1201/02, C12P21/02,
PC C1201/02, C12O1/02, C12O1/02, C12O1/03, C12N1/15, C12N13/50, G01N133/56, C12N15/00,
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ive 0; Mismatches 0
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/mol_type="genomic DNA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: JP 2002017378-A 4 22-JAN-2002;
PFIZER INC
OS Homo sapiens (human)
PN JP 2002017378-A/4
PD 22-JAN-2002
PP 05-APR-2001 JP 2001106882
PR 05-APR-2000 GB 0008504:3
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22-JAN-2002
05-APR-2001 JP 2001106882
05-APR-2000 GB 0008504:3
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Homo sapiens (human)
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                                                                      AAGAGAGAATTTTTCCCAATTGTATATTCTGATAATATTTTTCTGGGGAGTCTTGGGAAAT
                                                                                                         ATGGAACCAAATGGCACCTTCAGCAATAACAACAGCAGGAACTGCACAATTGAAAACTTC
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/product="putative G-protein coupled receptor"
/db xref="G1:20152270"
/db xref="G1:20152270"
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IIWLIPAASSIWLLDGGSEGNGSVTSCLELNIYKIAALQTMMYIALVVGCLLPFFTLS
ICYLLIIRVLLKVEVPESGLRVSHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWV
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                           /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="hGPCR21"
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IIWILIMASSIMLLDSGSEQNGSVTSCLELNIYKIAKLQTMNYTALVVGCLLPPFTLS
ICYLLIRVLKVVEVPESGLRVSHRKALTTIIITLIIPFLCFLPYHTLRTVHLTTWKV
GLCKDRLHKALVITLALAAANACFNPLLYYFAGENFKDRLKSALRKGHPQKAKTKCVF
PVSVWLRKETRV"
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Direct Submission
Submitted (11-APR-2000) Pharmacology, Univeristy of Virginia School
of Medicine, 1300 Jefferson Park Avenue, Charlottesville, VA 22908,
USA
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                                                                                                                         Eukaryott, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1041)
1 Heise, C. E., O'bowd, B.F., Figueroa, D.J., Sawyer, N., Nguyen, T., Im, D.S., Stocco, R., Bellefeuille, J.N., Abramovitz, M., Cheng, R., Coulombe, D.L. Jr., Zeng, Z., Liu, Q., Ma, L., Clements, M.K., Coulombe, N., Liu, Y., Austin, C.P., George, S.R., O'Neill, G.P., Metters, K.M., Lynch, K.R. and Evans, J.F.
Characterization of the human cysteinyl leukotriene 2 receptor J. Biol. Chem. 275 (39), 30531-30536 (2000)
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Best Local Similarity 100.0%; Pred. No. 3e-286;
Matches 993; Conservative 0; Mismatches 0;
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